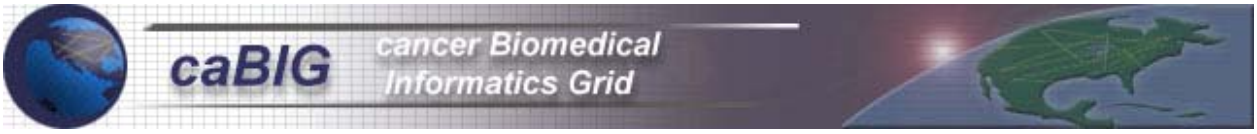


Integrative Cancer Research Special Interest Group Teleconference

Pathways SIG Meeting Minutes

Date, Time & Location:	May 4, 2004 1:00-2:00 EDT
Attendees:	Gary Bader – Sloan (funded developer, funded adopter) Terry Braun – Holden (funded developer) Ajay Jain – UC San Francisco (funded developer) Patrick McConnell – Duke (funded developer) Simon – Duke (funded developer) Cathy Wu – Georgetown (funded developer) Michelle Morris – Pittsburgh (unfunded adopter) Rakesh Nagarajan – Wash U (funded developer) Piers Nash – U of C (funded developer) John Rux – Wistar (funded adopter) Louise Showe – Wistar (funded adopter) Vincent Yau, Oregon Health (funded adopter) Naveen Vinukanda – Institute for Cancer Prevention (unfunded adopter) Edith Zang– Institute for Cancer Prevention (unfunded adopter) Carl Schaefer – NCICB Margo Sunshine – SRA Phan Winter – BAH Juli Klemm - BAH
Introduction:	**Roll-call, open meeting, review meeting goals** - Establish goals and priorities for this SIG - For match making purposes, Developers and Adopters will be asked to give a brief statement of their capabilities and interests, respectively - Identify and define additional research
Overview Discussion:	**Review goals and objectives of Pathways SIG** - View the SIG as a Steering Committee, guiding the activities of the WS in the area of Pathways - Group will discuss tools and data, as well as addressing needs **Open discussion of needs and interests** - Pathways can be a way of annotating genes and prioritizing candidates - There are many groups working on developing pathway data, tools and algorithms. It is important that tools and datasets can interact and that end-users can readily interact with them - Important to keep in mind the scientific questions that are being asked. The goal is often to take a large amount of data/information and put it into the context of something known, i.e. pathways. For example, a user may have microarray data on 40 different cell lines and want to know how players in pathways of interest are affected across these experiments. - There are different levels of pathway information: Membership, qualitative modeling, quantitative modeling/kinetics, visualization - There are a very large number of pathways data sources. Sloan has compiled a list of 118 sources: http://www.cbio.mskcc.org/prl/index.php.

	The team will review this list and add to it any other pathway resources of interest and look into posting this on the caBIG website. - Given the large number of data sources, it is important that they can be represented in a common data structure and that a non-redundant set of information can be created. - Many scientists feel that pathways curated by others are "wrong" – they do not represent their view of the pathway. Therefore, it is important to provide tools/language to curate pathways **Relevant standards** - PSI – Molecular interaction format, focused on protein-protein interactions - http://psidev.sourceforge.net/mi/xml/doc/user/ - BioPAX – Newly-created exchange format. v1.0 due to be released within a few weeks - http://www.biopax.org o Representations in the NCICB Pathway Interaction Tools were developed pre-BioPAX. Would move toward a standard such as BioPAX if one emerges o Is important that any standard have the ability to capture data available at various levels of granularity
High level review of Center interests in this SIG	**Developers** - Georgetown: PIR's iProClass database contains extensive functional annotation of proteins. For caBIG, they are interested in developing a caBIG-compatible framework for large-scale information retrieval - UC San Francisco: The QPACA tool allows one to project heterogeneous data onto pathways. Provides an analytical tool for measuring whether a set of genes is in a common pathway. Also provides methods for augmenting pathways. Interested in integrating this tool into caBIG. - Sloan: Has a suite of tools relevant to pathways: o BioPAX: Data exchange format for pathway information o cPath: Database focused on protein-protein interactions. Easy to install on a local machine. Could make available via a web-services API. Also, some content – curated pathways relevant to cancer. o Cytoscape: Tool for network visualization and analysis. Has a plug-in based architecture. Expression plug-in available. - NCICB: Pathway Interaction database. Stores pathway information from a variety of sources, provides a data retrieval tool. Provides visualization tool that allows molecules/interactions to be colored on the basis of expression. Currently contains KEGG and BioCarta pathways (BioCarta pathways are manually curated) – interested in adding more data sources. caBIO objects for pathway information are still being defined. - Holden: Interested in creating a more developer-friendly API for pathway data **Adopters** - Duke: Have both microarray and proteomics data - interested in tools to help make sense of this data in the context of pathways.

- Institute for Cancer Prevention: Have experience in DNA repair and signaling pathways. Have interest in BioPAX and Cytoscape.
- Oregon Health: Several of the tools are of interest. Important that tools are easily used by typical end-users (scientists and doctors).
- U of C: Interested in both database and visualization tools. Argonne has developed the WIT database, currently focused on prokaryotes. Would like to extend it to eukaryotes. Interested in peer-to-peer annotation exchange.
- Holden: Interested in better interfaces to pathway data
- Pittsburgh: Looking to the future, interested in modeling cancer cell populations.
- Wash U: Echos the interest of the other Adopters. Would like to integrate pathways tools and data with their system.
- Wistar: Interested in integrating microarray and proteomics data and organizing the results in the context of pathways. Need more comprehensive pathway data with standard representation.
- Dartmouth: Interested in integrating literature information into pathways database (text mining).
    - Wash U has a tool for creating literature-based networks. Is a part of Function Express for which a demo version will be available in a few weeks.

Summary: Developer tools seem to fit with Adopter needs, which are overlapping. To provide more information to Adopters:

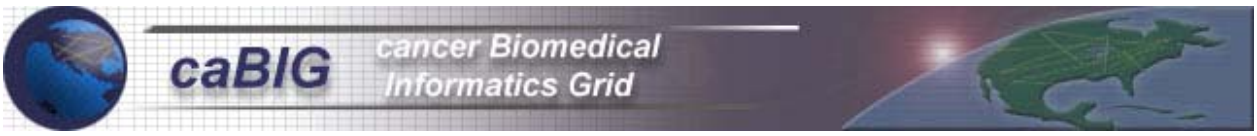
- Juli will send out detailed meeting minutes
- Developers will upload additional information on the caBIG on-line forum: **http://ncicbforums.nci.nih.gov/forums/cabigforum/lfs/icrlfs/SIGs/pathways**

Other discussion items:

- Gary Bader (Sloan) will draft a Mission Statement for this SIG.
- Team will aim to meet on the first Tuesday of each month at 1:00 Eastern if no conflicts are found.

Action Items:

Name Responsible	Action Item	Date Due	Notes
Send URL to Sloan's Pathway information resource to be posted in minutes	Gary Bader	(done)	Team will add to this as deemed necessary and post on the caBIG website.
Developers to post additional information relevant to their tools on the caBIG forum	All Developers	5/12/04	See URL in notes. If there is trouble posting, send information to Juli to post.
Draft Pathway SIG Mission Statement	Gary Bader	5/12/04	
Meeting Minutes	Juli Klemm	5/7/04	To be sent via email and posted on the caBIG forum.
Schedule next Pathways SIG meeting	Juli Klemm	5/14/04	



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